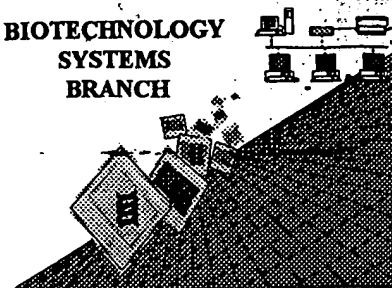


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0400
#4

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/645,593

Source: OIPF

Date Processed by STIC: 9/7/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED
SEP 20 2000
OIPF/JCW

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/645,593

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

P.7

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000
TIME: 14:27:09

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

Does Not Comply
Corrected Diskette Needed

OK
4 <110> APPLICANT: Chaudhary, Sarita
5 van Rooijen, Gijs
6 Moloney, Maurice
7 Singh, Surinder
9 <120> TITLE OF INVENTION: Flax Seed Specific Promoters
11 <130> FILE REFERENCE: 9369-147
13 <140> CURRENT APPLICATION NUMBER: US/09/645,593
14 <141> CURRENT FILING DATE: 2000-08-25
16 <150> PRIOR APPLICATION NUMBER: 60/151044
17 <151> PRIOR FILING DATE: 1999-08-27
19 <150> PRIOR APPLICATION NUMBER: 60/161,722
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000
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67 gcagcagccg aggtcttacc aggcggtgaa ggcggccact gcagccaccg cgggtggatc 2160
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000
 TIME: 14:27:09

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118 35 40 45
120 Val Leu Ser Gly Leu Ile Leu Thr Ala Thr Val Ile Ser Leu Ile Ile
121 50 55 60
123 Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Leu
124 65 70 75 80
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/645,593
 DATE: 09/07/2000
 TIME: 14:27:09

Input Set : A:\Sequence
 Output Set: N:\CRF3\09072000\I645593.raw

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000
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234      65      70      75      80
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237      85      90      95
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240      100     105     110
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286 aggggactgg agcgtgcaat cggccagatg aggcaggaca tccagcagca gggacagcag 1380
287 caggaagtig agaggtggtc ccatcaatct aaacaagtcg ctagggacct tccgggacag 1440

```

<210> 8
<211> 4999
<212> DNA
<213> Linum usitatissimum

see next page

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ctagtcttgt gaccatcctt cctcctgctc tagttgagag gccttgggac taacgagagg 180
tcagttggga tagcagatcc ttatcctgga ctagcctttc tgggtgtttca gagtcttcgt 240
gccgccgtct acatctatct ccattagggtc tgaagatgac tcttcacacc aacgacgttt 300
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cnattgtana	tggncgttg					4999

→ see
den 10
on
Error
summary
sheet

Please explain all n's in the sequence. The circled n's are a sample.

FSI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000
TIME: 14:27:10

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:412 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:414 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
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L:420 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000

TIME: 14:27:10

Input Set : A:\Sequence

Output Set: N:\CRF3\09072000\I645593.raw

L:455 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:455 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10